

Supplemental Information

Criteria for defining genomic overrepresentation and amplicons. Genes with copy number ratio > 1.40 (representing the upper 5% of the CGH ratios across all experiments) were considered to be overrepresented. A genomic fragment that contained six or more adjacent probes showing a copy number ratio > 1.40 , or a region with at least three adjacent probes with a copy number ratio > 1.40 and no less than one probe with a ratio > 2.0 , were considered to be amplicons. When indicated, the amplicon start and end positions were extended to symmetrically include 6 neighboring non-overrepresented probes (ratio < 1.40).

Relationship between genomic copy number and gene transcript level. The relationship between the levels of copy number and transcript changes was examined as described by Hyman et al (5). Briefly, within-slide normalized genome and transcript ratios in each cell line were log-transformed and median-centered; transcript data were also median-centered using values across 6 cell lines. For each gene, the CGH data were represented by a vector that was labeled "1" for genomic overrepresentation (including amplification) ratio greater than 1.40 and "0" for no genomic overrepresentation. Genomic copy number (including amplification) was correlated with transcript expression by using signal-to-noise statistics. A weight W was calculated for each gene: $W = (mg_1 - mg_0) / (rg_1 + rg_0)$, where mg_1 , rg_1 and mg_0 , rg_0 denote the means and standard deviations for the mRNA levels for genomic overrepresentation and non-

overrepresentation of the cell lines, respectively. To assess the statistical significance of each weight, 10,000 random permutations of the label vector were generated. The probability that a gene had a larger or equal weight by random permutation than the original weight was denoted by α . A low α (< 0.05) indicates a strong association between genomic overrepresentation and transcription.

Fig. 1S. 2D gel images of normal bronchial epithelial cells and lung adenocarcinoma cells (cell line H522). The red cycles indicate the up-regulated proteins in H522 cancer cell line.

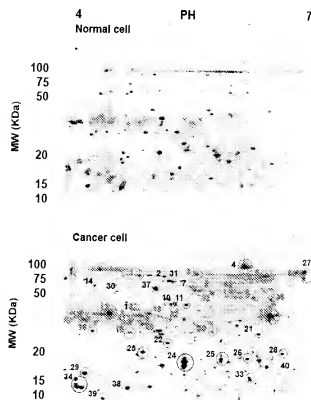


Fig. 2S. Cropped 2D gel images of selected proteins in normal bronchial epithelial cells and lung adenocarcinoma cells. Images were cropped from 2D gels of individual cell lines run between pH 4 and pH 7.

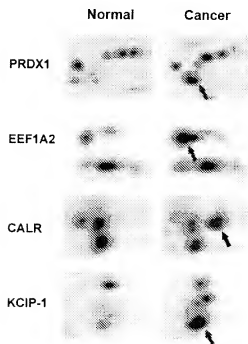


Fig. 3S. Confirmation by Southern, northern, and western blot analyses of increased DNA copies, transcript levels, and protein levels in the genes identified in high-throughput microarray and proteomic analyses revealed close correlations in the extent of changes in gene copies, transcript, and protein of each of the four genes in the cancer cell lines. Each experiment was repeated at least three times. Bars indicate SDs of the mean of three individual experiments.

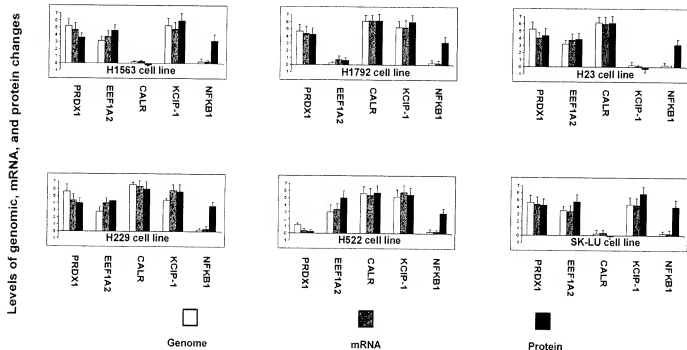


Fig. 4S. siRNAs against EEF1A2 or KCIP-1 specifically inhibit its expression, respectively. (A) Lung cancer cells were transfected with EEF1A2-siRNA, scrambled siRNA, or PBS. Western blot analysis of protein expression was performed 48 h after transfection. The same filter was probed with β -actin antibody to control for even loading. (B) Lung cancer cells were treated with KCIP-1 -siRNA, scrambled siRNA, or PBS. Western blot analysis of protein expression was performed 48 h after transfection.

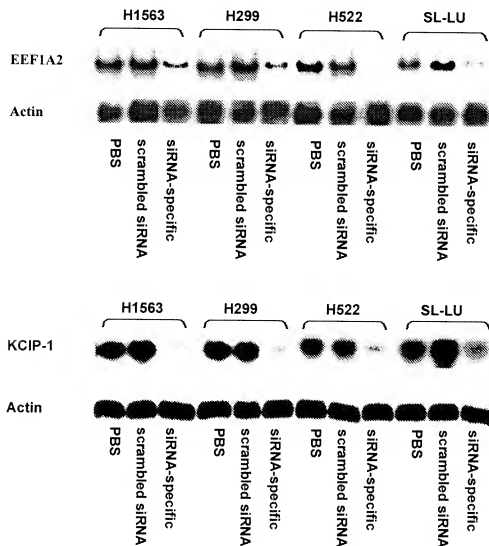


Fig. 5S. Effect of EEF1A2 or KCIP-1 depletion on cell proliferation. The viability of cells at 48 after transfection was determined by MTT staining to examine the effect of siRNA transfection on cancer cell proliferation. The growth rate was expressed as the percentage of viable EEF1A2-siRNA3-transfected cells (A) and KCIP-1-siRNA3-transfected cells (B) in relation to PBS-treated control cells and scrambled siRNA-treated cells. Bars indicate SDs of the mean of three individual experiments.

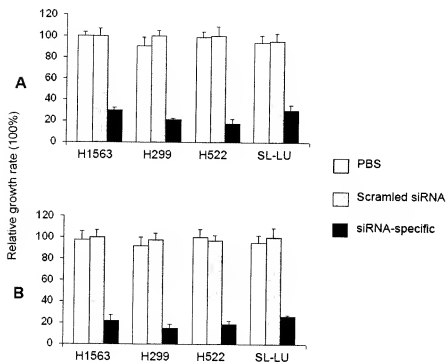


Fig. 6S. Survival analysis of 113 patients with stage 1 NSCLC based on EEF1A2 (left) and KCIP-1 (right) expression status.

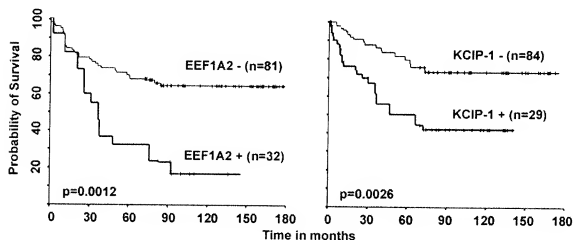


Table 1S. 587 genes with increases in DNA copy number detected by comparative genomic hybridization microarray in the lung adenocarcinoma cell lines

Genes with increased genome copy number		
Gene Symbol	Ch. loc.	Distance from p arm of chromosome (Mb)
ENO1	1	8.5
PINK1	1	20.1
DDOST	1	20.1
SMARCF1	1	26.3
SFN	1	26.4
NR0B2	1	26.5
EIF3S2	1	32.1
MLP	1	32.2
YARS	1	32.7
PDX1	1	45.4
AKR1A1	1	45.4
PRDX1	1	45.4
NASP	1	45.5
FAAH	1	46.2
UQCRH	1	46.2
RPL7	1	96.4
COL11A1	1	102.6
AMY2B	1	103.3
ECM1	1	147.3
MCL1	1	147.3
PSMB4	1	148.1
POGZ	1	148.2
S100A2	1	150.4
RAB13	1	150.7
JTB	1	150.7
RPS27	1	150.7
TPM3	1	150.9
HAX1	1	151
EFNA1	1	151.9
MUC1	1	151.9
PKLR	1	152

Clorf2	1	152
SCAMP3	1	152
PMF1	1	153
CCT3	1	153.1
MEF2D	1	153.2
CRABP2	1	153.4
PRCC	1	153.5
UAP1	1	159.2
TKT	1	159.3
ATP1B1	1	165.8
SLC19A2	1	166.1
F5	1	166.2
CHIT1	1	199.7
SNRPE	1	200.2
ACP1	2	0.255
ODC1	2	10.6 0
P5	2	10.9 0
CHST10	2	100.6 0
NPAS2	2	101.0 0
RPL31	2	101.2 0
MAP4K4	2	101.9 0
GCK	2	101.9 0
IL1R2	2	102.2 0
IL1RL2	2	102.4 0
NPHP1	2	110.4 0
BENE	2	110.4 0
BCL2L11	2	111.8 0
MERTK	2	112.6 0
RANBP2L1	2	113.0 0
SLC20A1	2	113.3 0
MGAT5	2	135.0 0
CCNT2	2	135.7 0
STAT1	2	191.8 0
STAT4	2	191.9 0
MYO1B	2	192.1 0
DNAH7	2	196.6 0
STK17B	2	197.0 0
SF3B1	2	198.2 0
PREI3	2	198.3 0

HSPE1	2	198.3 0
HSPD1	2	198.3 0
MYT1L	2	2.8 0
XRCC5	2	216.9 0
RPL37A	2	217.3 0
IGFBP5	2	217.5 0
IGFBP2	2	217.5 0
RNASEH1	2	3.2 0
RPS7	2	3.3 0
SOX11	2	5.8 0
IF	2	55.4 0
MTIF2	2	55.4 0
RPS27A	2	55.4 0
SLC1A4	2	65.2 0
RAB1A	2	65.3 0
ACTR2	2	65.4 0
RNF144	2	7.1 0
FABP1	2	88.3 0
RPIA	2	88.9 0
IGKC	2	89.0 0
ADAM17	2	9.6 0
YWHAQ	2	9.7 0
CCR2	3	46.2
LTF	3	46.3
MRAS	3	139.3
PIK3CB	3	139.7
COPB2	3	140.4
RBP1	3	140.5
RASA2	3	142.5
PFN2	3	151
SIAH2	3	151.7
H963	3	152.2
SMC4L1	3	161.4
KPNA4	3	161.5
B3GALT3	3	162.1
S100P	4	6.7
HMGE	4	7.1
ACOX3	4	8.5
CPZ	4	8.7

LIAS	4	39.3
UGDH	4	39.3
HIP2	4	39.5
FAP	4	39.8
ARHH	4	40
APBB2	4	40.7
UCHL1	4	41.1
IBSP	4	89.1
PKD2	4	89.3
SPP1	4	89.3
PET112L	4	153.1
TRIM2	4	154.7
PLRG1	4	155.9
FGG	4	156
FGB	4	156
SDHA	5	0.251
PDCD6	5	0.305
SEC6	5	0.479
SLC9A3	5	0.506
TRIP	5	0.926
TRIP13	5	0.926
CCT5	5	10.3
CTNND2	5	11
PTPRF	5	14.2
OSMR	5	38.9
FYB	5	39.1
C9	5	39.3
PTGER4	5	40.7
AAK1	5	40.8
RPL37	5	40.8
FOX D1	5	72.8
FOX D2	5	72.8
ENC1	5	74
HMGCR	5	74.7
KIF3A	5	132.1
QP-C	5	132.2
HSPA4	5	132.4
SPINK1	5	147.2
SPINK5	5	147.4

HTR4	5	147.8
MAML1	5	179.2
CANX	5	179.2
NQO2	6	3
E2F3	6	20.5
SOX4	6	21.7
HDGF	6	22.6
ITPR3	6	33.6
RPS10	6	34.6
TEF	6	35.4
RPL10A	6	35.4
RPA40	6	43.5
VEGF	6	43.7
CDC5L	6	44.4
SUPT3H	6	44.9
OSF-2	6	45.4
FSCN1	7	5.3
TRIAD3	7	5.4
MPP6	7	24.4
DFNA5	7	24.4
OSBPL3	7	24.5
CYCS	7	24.9
NFE2L3	7	25.9
HNRPA2B1	7	25.9
CBX3	7	25.9
ADCY1	7	45.3
IGFBP1	7	45.6
IGFBP3	7	45.7
HUS1	7	47.7
ZBPB	7	49.7
ZNFN1A1	7	50.1
DDC	7	50.2
WBSCR22	7	72.5
CLDN3	7	72.6
CLDN4	7	72.7
MDH2	7	75.3
HSPB1	7	75.5
DTX2	7	75.7
POMZP3	7	75.8

CALCR	7	92.7
CALR	7	92.7
GNGT1	7	93.1
TFPI2	7	93.1
BET1	7	93.2
COL1A2	7	93.6
ZFP95	7	98.7
ATP5J2	7	98.7
CYP3A5	7	98.8
CYP3A7	7	98.9
SI	7	133.6
AKR1B10	7	133.6
BPGM	7	133.7
RPS20	8	56.7
PENK	8	57.1
MET	8	57.1
LY96	8	74.6
TCEB1	8	74.6
PII5	8	75.5
LAPTM4B	8	98.5
MATN2	8	98.6
RPL30	8	98.7
POP1	8	98.8
UK114	8	98.8
STK3	8	99.1
COX6C	8	100.6
SPAG1	8	100.8
POLR2K	8	100.8
KCIP-1	8	101.6
PABPC1	8	101.78
CPN2	8	143.8
LY6H	8	144
EEF1D	8	144.4
TSTA3	8	144.5
VPS28	8	145.3
ZNF7	8	145.6
RPL8	8	145.6
PSMD5	9	117
TRAF1	9	117.1

TNF	9	117.1
TRA1	9	117.1
C5	9	117.2
CEP1	9	117.3
GOLGA1	9	121.1
RPL35	9	121.1
PPP6C	9	121.4
HSPA5	9	121.5
CIZ1	9	124.4
LCN2	9	124.4
GOLGA2	9	124.5
FUT7	9	133.4
ENTPD2	9	133.4
DPP7	9	133.4
PFKP	10	3.2
PITRM1	10	3.3
AKR1C4	10	5.1
AKR1C3	10	5.1
AKR1C1	10	5.1
CALML3	10	5.7
GDI2	10	6
CAMK2G	10	75.5
PLAU	10	75.6
ADK	10	75.8
DSP	10	76.7
VDAC2	10	76.9
TALDO1	11	0.434
DEAF1	11	0.503
KCNQ1	11	2.4
SLC22A1LS	11	2.9
SLC22A1L	11	2.9
TSSC3	11	2.9
TUB	11	8
EIF3S5	11	8
LMO1	11	8.2
RPL27A	11	8.7
ST5	11	8.8
SAA4	11	18.3
GTF2H1	11	18.4

LDHC	11	18.5
LDHA	11	18.5
CSRP3	11	19.2
HTATIP2	11	20.4
MAPK8IP1	11	45.9
HDAC2	11	46
OASIS	11	46.3
MDK	11	46.4
ARHGAP1	11	46.7
ROM1	11	62.6
B3GAT3	11	62.6
G2AN	11	62.6
EEF1G	11	62.6
BSCL2	11	62.7
STX5A	11	62.8
TAF6	11	62.8
POLR2G	11	62.8
AIP	11	67.5
DOC-1R	11	67.5
NDUFV1	11	67.6
GSTP1	11	67.6
ALDH3B2	11	67.7
MMP20	11	102.5
MMP8	11	102.6
MMP3	11	102.7
MMP10	11	102.7
MMP1	11	102.7
MMP13	11	102.8
MMP12	11	102.8
UPK2	11	118.9
G6PT1	11	118.9
HYOU1	11	118.9
SCNN1A	12	6.3
TNFRSF7	12	6.4
LTBR	12	6.4
NOL1	12	6.5
VAMP1	12	6.5
GAPD	12	6.5
GYS2	12	21.6

LDHB	12	21.7
KRT7	12	52.3
KRTHB3	12	52.4
KRTHB6	12	52.4
KRTHB1	12	52.4
KRTHB5	12	52.5
KRT5	12	52.6
KRT6E	12	52.6
IRS4	12	52.7
KRT2A	12	52.8
SOAT2	12	53.2
RAB5B	12	56.1
PA2G4	12	56.2
ERBB3	12	56.2
ATP5B	12	56.7
TEBP	12	56.8
NACA	12	56.8
PTPRR	12	70.7
TM4SF3	12	71.2
GPR49	12	71.6
CART	12	85.6
NTS	12	86.2
KITLG	12	88.8
KIT	12	88.8
ASCL1	12	103.3
TDG	12	104.3
NFYB	12	104.4
TXNRD1	12	104.6
CKAP4	12	106.6
MSI1	12	120.6
HSPC132	12	120.7
15E1.2	12	120.7
COX6A1	12	120.7
BGN	12	122.5
KNTC1	12	122.8
CD36	12	125
SCARB1	12	125
RAN	12	129.88
FZD9	12	130.4

RPL36A	14	48.1
SON	14	48.6
ATP5S	14	48.8
PGD	14	50.7
C14orf32	14	53.5
THBS2	15	37.5
SRP14	15	37.9
BUB1	15	38
BUB1B	15	38
IVD	15	38.3
TRAF4	15	38.3
C18B11	15	38.4
GCHFR	15	38.6
RAD51	15	38.6
SPINT1	15	38.7
CIB1	15	40.2
RPL17	15	45.26
SLC12A1	15	46.1
NR2E3	15	69.7
PKM2	15	70.1
AP3S2	15	88
IDH2	15	88.2
MRPL28	16	0.357
RPL23A	16	0.377
SOLH	16	0.518
PIGQ	16	0.56
RAB40C	16	0.58
MSLN	16	0.753
BAIAP3	16	1.3
UBE2I	16	1.3
CLCN7	16	1.4
MAPK8IP3	16	1.7
IGFALS	16	1.8
HAGH	16	1.8
RPL3L	16	1.9
RPS2	16	1.95
SYNGR3	16	2
MMPL1	16	3.1
CLDN9	16	3.1

PM5	16	16.3
RPS15A	16	18.7
ARL6IP	16	18.7
COQ7	16	19
GTF3C1	16	27.4
EIF3S8	16	28.3
ATP2A1	16	28.9
CD19	16	28.9
TUFM	16	28.9
TBX6	16	30.1
ALDOA	16	30.1
NME4	16	53.6
CCL17	16	57.2
GPR56	16	57.4
KIFC3	16	57.5
CDH1	16	68.5
SNTB2	16	69
NQO1	16	69.5
AARS	16	70
DDX19	16	70.1
SLC7A5	16	87.6
CA5A	16	87.7
MVD	16	88.4
CYBA	16	88.4
CBFA2T3	16	88.6
APRT	16	88.6
GALNS	16	88.6
CDH15	16	88.9
RPL13	16	89.3
MCP	17	32.4
AATF	17	35
ERBB2	17	35.11
TOP2A	17	38.5
CCR7	17	38.6
KRT12	17	38.8
KRT10	17	38.8
KRT20	17	38.9
KRTHA3A	17	39.4
KRTHA4	17	39.4

KRTHA3B	17	39.4
KRTHA5	17	39.5
KRTHA7	17	39.5
KRTHA1	17	39.5
KRTHA2	17	39.5
KRT16	17	39.5
KRT14	17	39.5
KRT17	17	39.5
KRT9	17	39.6
KRT13	17	39.6
KRT15	17	39.6
KRT19	17	39.6
HAP1	17	39.8
JUP	17	39.8
ACLY	17	39.9
CRF	17	40.39
PSME3	17	40.9
BECN1	17	40.9
G6PC	17	41
ARHN	17	41.1
RPL27	17	41.1
NME1	17	46.59
SCAP1	17	46.6
HOXB1	17	46.9
HOXB5	17	47
HOXB7	17	47
HOXB3	17	47
HOXB2	17	47
HOXB13	17	47.1
ATP5G1	17	47.3
PHB	17	47.8
ITGA3	17	48.5
SGCA	17	48.6
COL1A1	17	48.6
CHAD	17	48.9
CAV3	17	49
CACNA1G	17	49
ABCC3	17	49.1
TOB1	17	49.3

NME2	17	49.6
TOM1	17	53.3
TOM1L1	17	53.3
COX11	17	53.4
RPL38	17	72.7
SLC9A3R1	17	73.2
FDXR	17	73.3
ATP5H	17	73.5
SMT3H2	17	73.6
MSF	17	75.7
EVER1	17	76.6
TK1	17	76.6
SYNGR2	17	76.6
BIRC5	17	76.7
LGALS3BP	17	77.4
CBX4	17	78.4
MRPL12	17	80.2
PDE6G	17	80.2
P4HB	17	80.3
PCYT2	17	80.4
TGIF	18	3.4
NAPG	18	10.5
IMPA2	18	12
AFG3L2	18	12.3
PTPN2	18	12.8
CDH2	18	25.4
DSC3	18	28.5
DSG1	18	28.8
DSG3	18	28.9
DSG2	18	29
B4GALT6	18	29.1
TTR	18	29.1
MEP1B	18	29.7
PPAP2C	19	0.221
PEPD	19	38.6
GPI	19	39.55
ZNF135	19	39.8
ZNF140	19	39.8
SCN1B	19	40.2

HPN	19	40.2
ZNF146	19	41.4
ZNF345	19	42
DPF1	19	43.4
SPINT2	19	43.4
PSMD8	19	43.5
YIF1P	19	43.5
RYS1	19	43.6
SUPT5H	19	44.6
RPS16	19	44.6
BCKDHA	19	46.6
CEACAM4	19	46.8
CEACAM5	19	46.9
CEACAM6	19	46.9
CEACAM3	19	47
ATP1A3	19	47.1
RABAC1	19	47.1
GPR4	19	50.8
EML2	19	50.8
GPR19	19	50.8
GIP	19	50.8
GIPR	19	50.8
SNRPD2	19	50.9
PSCD2	19	53.6
GRIN2D	19	53.6
KDELRL	19	53.6
TNNI3	19	60.3
TNNT1	19	60.3
PTPRH	19	60.4
SYT5	19	60.4
IL11	19	60.6
RPL28	19	60.6
PEG3	19	61.9
STK13	19	62.4
ZNF272	19	62.5
SEDLP	19	62.6
ZNF211	19	62.8
ZNF134	19	62.8
ZNF154	19	62.9

ZNF274	19	63.4
ZNF8	19	63.5
ZNF132	19	63.6
RPS5	19	63.6
UBE2M	19	63.7
TRIM28	19	63.7
SRC	20	35.4
DAP	20	35.6
TGIF2	20	35.8
KIAA1219	20	37.8
TOP1	20	40.3
UBE2C	20	45.1
PRKCBP1	20	46.5
SS18L1	20	61.4
CDK3	20	61.6
RPS21	20	61.6
EEF1A2	20	62.8
URKL1	20	63.3
C20orf14	20	63.3
MYT1	20	63.5
TFF3	21	42.6
TFF2	21	42.7
TFF1	21	42.7
PDXK	21	44
CSTB	21	44.1
MIF	22	22.6
CHEK2	22	27.4
CDS1	22	27.4
XBP1	22	27.5
LGALS1	22	36.4
PRDX4	X	22.9
PFC	X	46.3
SYN1	X	46.3
TIMP1	X	46.3
PIM2	X	47.6
JM4	X	47.7
JM5	X	47.7
T54	X	47.8
LMO6	X	47.8

PLP2	X	47.8
AKAP4	X	48.7
MAGED1	X	50.3
PHKA1	X	70
RPS4X	X	71
COX7B	X	75.2
ATP7A	X	75.3
PGK1	X	75.4
GPR23	X	76.1
SSR4	X	152.6

Table 2S. Summary of amplicons in 6 lung adenocarcinoma cell lines by CGH microarray

Location	Start from p arm of each chromosome (Mb)	End from p arm of each chromosome (Mb)	Size of the Amplicon (bp)
1p36.23	7,935,153	8,990,392	1,055,239
1p36.11	26,706,664	26,924,602	217,938
1p34.1	45,645,801	45,753,660	107,859
1q21.33	150,346,660	153,583,682	3,237,022
1q24.2	165,807,605	166,287,379	479,774
2p25.1	3,116,230	5,792,115	2,675,885
2p25.1	9,580,011	10,903,558	1,323,547
2p11.2	88,261,772	89,459,144	1,197,372
2q11.2	100,895,131	102,103,403	1,208,272
2q32.3-33.1	191,800,000	198,190,504	6,390,504
2q35	216,797,696	217,354,662	556,966
3q22.3	139,549,237	140,591,166	1,041,929
3q25.1	151,165,392	152,403,677	1,238,285
3q25.33	161,600,132	162,305,862	705,730
4p16.1	6,812,868	8,739,550	1,926,682
4q22.2	89,077,881	89,253,981	176,100
5p15.33	271,401	971,160	699,759
5p15.2	10,303,371	17,329,943	7,026,572
5p13.1	38,881,893	40,871,072	1,989,179
5q32	147,184,339	148,013,909	829,570
5q35.3	180,348,507	180,603,502	254,995
6p22.3	20,510,377	22,679,871	2,169,494
6p21.33	2,945,207	3,102,759	157,552

7p22.1	5,405,698	6,296,940	891,242
7p15.3	24,386,241	26,026,216	1,639,975
7p13	45,701,327	47,792,486	2,091,159
7q11.23	72,542,549	75,901,214	3,358,665
7q21.3	93,159,360	93,705,195	545,835
8q22.3	98,856,461	101,804,115	2,947,654
8q24.3	145,619,808	146,043,698	423,890
9p22.1	19,366,254	21,132,144	1,765,890
9p13.3	33,230,196	33,392,517	162,321
9q33.2	120,657,888	121,019,442	361,554
9q33.3	124,720,183	125,083,163	362,980
9q34.11	127,991,272	128,117,822	126,550
10p15.2	3,099,712	3,205,003	105,291
10p15.1	5228798	5,895,379	666,581
11p15.5	2,422,797	2,907,226	484,429
11p15.4	8,016,756	8,889,074	872,318
11p-15.1	18,209,479	20,361,904	2,152,425
11p11.2	45,863,778	46,678,696	814,918
11q12.3	62,139,345	62,356,136	216,791
11q13.2	67,030,545	67,198,753	168,208
11q21	93,866,801	93,872,392	5,591
12p13.31	6,326,276	6,547,680	221,404
12q13.13	51,148,575	54,782,854	3,634,279
12q23.2	101,853,931	105,144,375	3,290,444
12q24.31	123,787,056	123,873,214	86,158
14q21.3	49,155,159	49,872,026	716,867
15q14	37,660,567	38,937,145	1,276,578
15q23	69,889,948	70,310,738	420,790

15q23	45,268,852	45,272,849	3,997
15q26.1	88,177,793	88,446,712	268,919
16p13.3	357,397	1,984,277	1,626,880
16p13.3	3,002,207	3,004,507	2,300
16q13.2	9,762,923	10,184,112	421,189
16p12.3	18,418,684	18,998,855	580,171
16p11.2	29,989,236	30,004,583	15,347
16p21.31	34,493,211	35,546,536	1,053,325
16q22.2	68,300,807	68,890,598	589,791
16q24.2-24.3	86,421,130	88,158,450	1,737,320
17q21.2	35,798,321	37,328,798	1,530,477
17q21.31	38,215,678	41,268,973	3,053,295
17q21.33	44,836,419	46,604,103	1,767,684
17q21.33-q22	50333203	50,401,053	67,850
17q25.1	69,711,412	70,380,692	669,280
17q25.2	72,789,117	73,732,372	943,255
17q25.3	74,478,932	75,427,826	948,894
17q25.3	77,227,655	77,462,586	234,931
18p11.21	10,516,031	12,874,334	2,358,303
18q12.1	23,784,934	28,054,365	4,269,431
18q12.1	45,268,852	45,272,849	3,997
19q13.13	12,910,423	12916303	5,880
19q13.1	38,569,699	40,249,315	1,679,616
19q13.12-13.2	41,411,488	43,770,012	2,358,524
19q13.2	44,618,478	44,628,052	9,574
19q13.2	46,595,544	47,155,320	559,776
19q13.32	50,863,342	50,887,282	23,940

19q13.32	53,589,944	53,674,457	84,513
19q13.42-13.43	60,354,950	63,753,894	3,398,944
20q13.12	43,874,662	45,418,974	1,544,312
20q13.33	60,152,217	62,377,837	2,225,620
21q22.3	42,605,233	44,020,687	1,415,454
22q12.1	22,561,118	27,521,114	4,959,996
Xp22.11	21,810,216	23,464,172	1,653,956
XP11.23	47,187,558	48,787,809	1,600,251
xP11.22	49,658,442	51,478,486	1,820,044
Xq13.1	71,280,162	71,583,499	303,337
Xq21.1	71,280,162	77,818,738	6,538,576
Xq28	152,579,818	152,584,801	4,983

Table 3S. 587 genes with increased mRNA levels detected by transcript microarray in the lung adenocarcinoma cell lines

Gene Symbol	Chro.	Distance from p arm of chromosome (Mb)
ENO1	1	8.5
DDOST	1	20.1
SFN	1	26.4
MLP	1	32.2
AKR1A1	1	45.4
PRDX1	1	45.4
UQCRH	1	46.2
PABPN1	1	57.1
RPL7	1	96.4
COL11A1	1	102.6
TRIM29	1	113.1
KLF6	1	114.7
MCL1	1	147.3
PCSK2	1	147.8
PSMB4	1	148.1
S100A2	1	150.4
CALD1	1	150.5
JTB	1	150.7
RPS27	1	150.7
HAX1	1	151
MUC1	1	151.9
NQO3A2	1	152.5
CCT3	1	153.1
CRABP2	1	153.4
TKT	1	159.3
ATP1B1	1	165.8
CHIT1	1	199.7
SNRPE	1	200.2
IRS2	1	203.9
FBLN1	1	204.3
MGC9850	1	214.9
YWHAQ	2	9.6
TNNI2	2	26.3

USP9Y	2	26.9
TGFBR1	2	38.7
WNT6	2	74
GLRX	2	177.9
FAS	2	191.7
ODC1	2	10.6 0
RPL31	2	101.2 0
BENE	2	110.4 0
CCT2	2	135.7 0
STAT1	2	191.8 0
HSPD1	2	198.3 0
HSPE1	2	198.3 0
RPL37A	2	217.3 0
IGFBP2	2	217.5 0
RPS7	2	3.3 0
RAB1A	2	65.3 0
IGKC	2	89.0 0
LTF	3	46.3
PSMF1	3	52.7
HOXD9	3	101.9
UMPS	3	150.6
PFN2	3	151
KPNA4	3	161.5
S100P	4	6.7
UGDH	4	39.3
UCHL1	4	41.1
SPP1	4	89.3
EML1	4	104.1
PLAT	4	143.3
TRIM2	4	154.7
FGB	4	156
FGG	4	156
MFGE8	4	186.7
SDHA	5	0.251
PDCD6	5	0.305
CCT5	5	10.3
PTPRF	5	14.2
RPL37	5	40.8

SIAT4C	5	64.1
ENC1	5	74
QP-C	5	132.2
GTF2E1	5	132.4
BLZF1	5	133.3
RABGGTB	5	133.7
SPINK1	5	147.2
XRCC3	5	178.1
CRSP9	5	179.1
CANX	5	179.2
PMS2L1	5	198.2
SOX4	6	21.7
EFNB2	6	21.7
HDGF	6	22.6
RPS10	6	34.6
RPL10A	6	35.4
RAD23A	6	38.8
VEGF	6	43.7
OSF-2	6	45.4
DRCTNNB1A	6	64.3
ABCF1	6	159.2
FSCN1	7	5.3
FBXO11	7	5.3
CYCS	7	24.9
CG018	7	24.9
METAP2	7	24.9
CBX3	7	25.9
CRYBA1	7	26
TFCP2	7	43.9
IGFBP3	7	45.7
PLK3	7	72.7
CLDN4	7	72.7
HSPB1	7	75.5
CALR	7	92.7
PDAP1	7	93.1
COL1A2	7	93.6
ATP5J2	7	98.7
AKR1B10	7	133.6

SIAT7B	7	140.9
RPS20	8	56.7
ZW10	8	61.6
TCEB1	8	74.6
LAPTM4B	8	98.5
RPL30	8	98.7
GGTL4	8	100.9
PARD6A	8	101.2
KCIP-1	8	101.6
PABPC1	8	101.78
LY6E	8	143.9
EEF1D	8	144.4
TSTA3	8	144.5
RPL8	8	145.6
RPA1	9	19.4
ALDH3A2	9	36.8
SF3B2	9	38.4
7-Sep	9	72.8
ACTA2	9	72.9
TRA1	9	117.1
RPL35	9	121.1
HSPA5	9	121.5
LCN2	9	124.4
OAZIN	9	130.3
DPP7	9	133.4
PFKP	10	3.2
AKR1C1	10	5.1
PLAU	10	75.6
DSP	10	76.7
CBLB	10	123.2
TALDO1	11	0.434
CLTCL1	11	1.7
SLC22A1L	11	2.9
TSSC3	11	2.9
RPL27A	11	8.7
ST5	11	8.8
SAA1	11	116.6
MYOZ1	11	18.4

LDHA	11	18.5
ALDOA	11	33.7
MDK	11	46.4
EEF1G	11	62.6
REG1B	11	66.9
DOC-1R	11	67.5
GSTP1	11	67.6
DPEP1	11	95.1
MMP7	11	102.4
MMP12	11	102.8
GAB2	11	109.6
HYOU1	11	118.9
EHD3	12	1.6
SCNN1A	12	6.3
KRT8	12	51.6
KRT18	12	51.6
KRT7	12	52.3
KRT5	12	52.6
KRT6E	12	52.6
HADHA	12	55
ERBB3	12	56.2
NACA	12	56.8
RAB14	12	67.3
TM4SF3	12	71.2
NTS	12	86.2
CHAD	12	103.2
ASCL1	12	103.3
TXNRD1	12	104.6
CKAP4	12	106.6
COX6A1	12	120.7
BGN	12	122.5
RAN	12	129.88
RPL36A	14	48.1
PGD	14	50.7
MPZ	14	61.2
THBS2	15	37.5
TRAF4	15	38.3
SPINT1	15	38.7

RGN	15	42.8
RPL17	15	45.26
PKM2	15	70.1
CYFIP2	15	76.6
KIF21B	15	87.8
IDH2	15	88.2
RPL23A	16	0.377
MSLN	16	0.753
UBE2I	16	1.3
RPS2	16	1.95
CLDN9	16	3.1
ARL6IP	16	18.7
OSBPL1A	16	18.7
EIF3S8	16	28.3
TUFM	16	28.9
ALDOA	16	30.1
NME4	16	53.6
GPR56	16	57.4
CDH1	16	68.5
NQO1	16	69.5
SLC7A5	16	87.6
APRT	16	88.6
GALNS	16	88.6
RPL13	16	89.3
ARAF	17	4.7
PELO	17	19.6
MCP	17	32.4
ERBB2	17	35.11
KRT17	17	39.5
KRT19	17	39.6
JUP	17	39.8
CRF	17	40.39
RPL27	17	41.1
NME1	17	46.59
COL1A1	17	48.6
ABCC3	17	49.1
NME2	17	49.6
CLDN5	17	53.7

DCBLD2	17	71.4
RPL38	17	72.7
SMT3H2	17	73.6
SYNGR2	17	76.6
LGALS3BP	17	77.4
P4HB	17	80.3
PPAP2C	19	0.221
CD81	19	0.8
GPI	19	39.55
HPN	19	40.2
ZNF146	19	41.4
SPINT2	19	43.4
PSMD8	19	43.5
YIF1P	19	43.5
RPS16	19	44.6
SYNGR3	19	44.6
CEACAM5	19	46.9
CEACAM6	19	46.9
FOXP1	19	46.9
TUBE1	19	46.9
GIPR	19	50.8
SNRPD2	19	50.9
KDELRL1	19	53.6
CAT	19	60.6
RPL28	19	60.6
RPS5	19	63.6
TRIM28	19	63.7
DAP	20	35.6
TOP1	20	40.3
LIPC	20	42.9
UBE2C	20	45.1
RAP2A	20	56.8
RPS21	20	61.6
EEF1A2	20	62.8
TFF3	21	42.6
TFF1	21	42.7
CSTB	21	44.1
FALZ	21	46.3

NR4A1	22	21.2
MIF	22	22.6
XBP1	22	27.5
DDX18	22	38.2
PRDX4	X	22.9
SYN1	X	46.3
TIMP1	X	46.3
LOC152185	X	47.2
PLP2	X	47.8
MAGED1	X	50.3
RPS4X	X	71
PGK1	X	75.4
RANBP1	X	77.2
SSR4	x	152.6

Table 4S. Sequences of the siRNAs.

EEF1A2mRNA sequence (NM_001958)	Antisense siRNA Oligonucleotide Template 5'AATAGGTGGACCCCCTCCCGGCCTGTCTC3'
	Sense siRNA Oligonucleotide Template 5'AACCGGGAGGGGGTCCACCTACCTGTCTC3'

KCIP-1 mRNA sequence (NM_003406)	Antisense siRNA Oligonucleotide Template 5'AACCCTGGGGACTACGACGTCCCTGTCTC3'
	Sense siRNA Oligonucleotide Template 5'AAGACGTCGTAGTCCCCAGGGCCTGTCTC3'